

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,732

DATE: 07/24/2001

TIME: 10:39:04

Input Set : A:\57453c1.app

Output Set: N:\CRF3\07242001\I899732.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Salon et al, John A.
 5 <120> TITLE OF INVENTION: DNA Encoding A Human Melanin Concentrating Hormone
 6 Receptor (MCH1) And Uses Thereof
 8 <130> FILE REFERENCE: 1795/57453-C/JPW
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/899,732
 11 <141> CURRENT FILING DATE: 2001-07-05
 13 <150> PRIOR APPLICATION NUMBER: 09/610,635
 14 <151> PRIOR FILING DATE: 2000-07-05
 16 <160> NUMBER OF SEQ ID NOS: 28
 18 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

375 <210> SEQ ID NO: 16
 376 <211> LENGTH: 100
 377 <212> TYPE: PRT
 378 <213> ORGANISM: Artificial Sequence
 380 <220> FEATURE:
 381 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
 E--> 382 MCH1
 W--> 384 <210> SEQ ID NO:
 W--> 384 <211> LENGTH:
 W--> 384 <212> TYPE:
 W--> 384 <213> ORGANISM:
 384 <400> SEQUENCE: 16
 E--> 385 Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu
 386 1 5 10 15
 388 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
 389 20 25 30
 391 Cys Gly Ala Cys Ala Pro Gly Gln Gly Arg Arg Trp Arg Leu Pro
 392 35 40 45
 394 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 395 50 55 60
 397 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 398 65 70 75 80
 400 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
 401 85 90 95
 403 Gly Ser Pro Pro
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 407 <210> SEQ ID NO: 17
 408 <211> LENGTH: 100
 409 <212> TYPE: PRT
 410 <213> ORGANISM: Artificial Sequence
 412 <220> FEATURE:
 413 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human
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W--> 416 <210> SEQ ID NO:

W--> 416 <211> LENGTH:

W--> 416 <212> TYPE:

W--> 416 <213> ORGANISM:

416 <400> SEQUENCE: 17

E--> 417 Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
 418 1 5 10 15
 420 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
 421 20 25 30
 423 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
 424 35 40 45
 426 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 427 50 55 60
 429 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 430 65 70 75 80
 432 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
 433 85 90 95
 435 Gly Ser Pro Pro
 436 100

535 <210> SEQ ID NO: 26

536 <211> LENGTH: 422

537 <212> TYPE: PRT

538 <213> ORGANISM: Artificial Sequence

540 <220> FEATURE:

541 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human

E--> 542 MCH1

W--> 544 <210> SEQ ID NO:

W--> 544 <211> LENGTH:

W--> 544 <212> TYPE:

W--> 544 <213> ORGANISM:

544 <400> SEQUENCE: 26

E--> 545 Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
 546 1 5 10 15
 548 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
 549 20 25 30
 551 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
 552 35 40 45
 554 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
 555 50 55 60
 557 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
 558 65 70 75 80
 560 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
 561 85 90 95
 563 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
 564 100 105 110
 566 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
 567 115 120 125
 569 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
 570 130 135 140

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572 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
573 145                               150                               155                               160
575 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
576                               165                               170                               175
578 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
579                               180                               185                               190
581 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
582                               195                               200                               205
584 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
585                               210                               215                               220
587 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
588 225                               230                               235                               240
590 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
591                               245                               250                               255
593 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
594                               260                               265                               270
596 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
597                               275                               280                               285
599 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
600                               290                               295                               300
602 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
603 305                               310                               315                               320
605 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
606                               325                               330                               335
608 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
609                               340                               345                               350
611 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
612                               355                               360                               365
614 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
615                               370                               375                               380
617 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
618 385                               390                               395                               400
620 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
621                               405                               410                               415
623 Thr Glu Ser Lys Gly Thr
624                               420

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627 <210> SEQ ID NO: 27

628 <211> LENGTH: 422

629 <212> TYPE: PRT

630 <213> ORGANISM: Artificial Sequence

632 <220> FEATURE:

633 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human

E--> 634 MCH1

W--> 636 <210> SEQ ID NO:

W--> 636 <211> LENGTH:

W--> 636 <212> TYPE:

W--> 636 <213> ORGANISM:

636 <400> SEQUENCE: 27

E--> 637 Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu

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638      1          5          10          15
640 Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
641          20          25          30
643 Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
644          35          40          45
646 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
647          50          55          60
649 Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
650 65          70          75          80
652 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
653          85          90          95
655 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
656          100          105          110
658 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
659          115          120          125
661 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
662          130          135          140
664 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
665 145          150          155          160
667 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
668          165          170          175
670 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
671          180          185          190
673 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
674          195          200          205
676 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
677          210          215          220
679 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
680 225          230          235          240
682 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
683          245          250          255
685 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
686          260          265          270
688 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
689          275          280          285
691 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
692          290          295          300
694 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
695 305          310          315          320
697 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
698          325          330          335
700 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
701          340          345          350
703 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
704          355          360          365
706 Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
707          370          375          380
709 Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
710 385          390          395          400

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712 Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
 713 405 410 415

715 Thr Glu Ser Lys Gly Thr
 716 420

719 <210> SEQ ID NO: 28

720 <211> LENGTH: 353

721 <212> TYPE: PRT

722 <213> ORGANISM: Artificial Sequence

724 <220> FEATURE:

725 <223> OTHER INFORMATION: Description of Artificial Sequence: mutated human

E--> 726 MCH1

W--> 728 <210> SEQ ID NO:

W--> 728 <211> LENGTH:

W--> 728 <212> TYPE:

W--> 728 <213> ORGANISM:

728 <400> SEQUENCE: 28

E--> 729 Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly Pro Asn Ala Ser Asn
 730 1 5 10 15
 732 Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
 733 20 25 30
 735 Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
 736 35 40 45
 738 Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
 739 50 55 60
 741 Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
 742 65 70 75 80
 744 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
 745 85 90 95
 747 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
 748 100 105 110
 750 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
 751 115 120 125
 753 Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
 754 130 135 140
 756 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
 757 145 150 155 160
 759 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
 760 165 170 175
 762 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
 763 180 185 190
 765 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
 766 195 200 205
 768 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
 769 210 215 220
 771 Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala
 772 225 230 235 240
 774 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
 775 245 250 255
 777 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr

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Input Set : A:\57453c1.app

Output Set: N:\CRF3\07242001\I899732.raw

```

778                260                265                270
780 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
781                275                280                285
783 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
784                290                295                300
786 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
787 305                310                315                320
789 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala
790                325                330                335
792 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
793                340                345                350
795 Thr

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/899,732

DATE: 07/24/2001

TIME: 10:39:05

Input Set : A:\57453c1.app

Output Set: N:\CRF3\07242001\I899732.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:382 M:252 E: No. of Seq. differs, <211>LENGTH:Input:100 Found:0 SEQ:16
L:384 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:384 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:414 M:252 E: No. of Seq. differs, <211>LENGTH:Input:100 Found:0 SEQ:17
L:416 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:416 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:542 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:0 SEQ:26
L:544 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:544 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:634 M:252 E: No. of Seq. differs, <211>LENGTH:Input:422 Found:0 SEQ:27
L:636 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:636 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:726 M:252 E: No. of Seq. differs, <211>LENGTH:Input:353 Found:0 SEQ:28
L:728 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:728 M:282 W: Numeric Field Identifier Missing, <213> is required.